**LOBSTER Cheat Sheet**

**Initialize**

**>>** cd('E:/LOBSTER') Note: change string by actual LOBSTER installation folder

**>>** init

**Calling jobs**

**>>** JobName (only work if located in current folder or LOBSTER\_ROOT/Jobs folder)

Jobs can also be launched by opening \*.m files and pressing green arrow in script editor

**Calling journals**

|  |  |
| --- | --- |
| >> JENI; | Journal browser |
| >> JENI('Tissue\_SegWaterTiles.jl');\* | Specify journal |
| >> GENI('Tissue\_SegWaterTiles.jl'); | No image display |
| >> [InputFolder MaskFolder] = JENI('Tissue\_SegWaterTiles.jl'); | Retrieve folders |
| >> JENI('Tissue\_SegWaterTiles.jl', InputFolder, MaskFolder); | Force folders |
| >> JENI('FISH\_sptdet.jl','','',{'\*\_C01\*.tif','\*\_C02\*.tif'}); | Replace string |
| >> JENI('Tissue\_SegWaterTiles.jl', InputFolder, N);\*\* | Force In, local out |

**\***if journal not located in Journals folder, specify path ('E:/MyJournals/Tissue\_SegWaterTiles.jl').

**\*\***local output located at: InputFolder /.. / InputFolder(N) (N > 0)

InputFolder /.. /../ InputFolder(-N) (N < 0)

**Measurements**

|  |  |
| --- | --- |
| >> IRMA(MaskFolder, ReportFolder, Meas, Dim, ZRatio);\* | Simple call |
| >> ReportFolder = IRMA(MaskFolder, '.', Meas, Dim, ZRatio); | Retrieve folder |
| >> ReportFolder = IRMA(MaskFolder, N, Meas, Dim, ZRatio);\*\* | Local out |
| >> IRMA(MaskFolder, ReportFolder, Meas, Dim, ZRatio, InputFolder, '\*C01\*.tif'); | Int. meas. |
| >> IRMA(…, '\*C01\*.tif', '\*C02\*.tif'); | Int. meas. |
| >> IRMA(MaskFolder2, '.', 'Objs', Dim, ZRatio, MaskFolder1, '\*dst\*'); | Distance meas. |

\***Meas**: 'Objs', 'Spts', 'Skls', 'Trks' or 'Spst' ; **Dim**: 2 or 3 ; **ZRatio**: Z aspect ratio

\*\*local output located at: MaskFolder /.. / MaskFolder(N) (N > 0)

MaskFolder /.. /../ MaskFolder(-N) (N < 0)

**Note**: ReportFolder can also be set to '' (none) or '.' (ROOT/Results/Reports/MaskFolder)

**Exportation (IRMA)**

|  |  |
| --- | --- |
| >> IRMA(MaskFolder, '.', 'Objs', 3 , {ZRatio, Smp , '.'} );\* | 3D Object surfaces (STL) |
| >> IRMA( MaskFolder, '.', 'Skls', 3 , {ZRatio, Stp, '.'} ); | 3D Filament centerlines (SWC) |
| >> IRMA( MaskFolder, '.', 'Trks', 2, {ZRatio, '', '.'} );\*\* | 2D tracks (SWC) |

\***Smp**: mesh sampling ratio (0.1: low details – 1: full details)

\*\***Stp**: Network tracing step (pixels, typically in range 2 - 4)

**Exportation (JOSE)**

|  |  |
| --- | --- |
| >> JOSE(InputFolder,'\*C00\*' ,ReportFolder,'Objs',ExportFolder,'IJ', Flags, '');\* | SceneViewer |
| >> JOSE( InputFolder1, '\*C00\*', InputFolder2, '\*C01\*', ReportFolder1, 'Objs',  ReportFolder2, 'Spts', ExportFolder, 'IJ', Flags, ''); | SceneViewer |
| >> ColorCode = '(getResult("Area",ObjIdx) >= 250)+(getResult("Area",ObjIdx) >= 350)';  >> JOSE( InputFolder,'\*\_C00\*',ReportFolder,'Objs',ExportFolder, 'IJ', Flags, ColorCode ); | Boxes  color-coding |
| >> JOSE( ReportFolder, 'Spts', ExportFolder, 'CellInsight', '', '' );\*\* | CellInsight |

**Flags:** 3 digit 0/1 flags (Channel Step + FoldersIn + Time-lapse, e.g. 100)

\*Displayed items in pairs: images/annotations folder + image filter/annotation type

\*\*ExportFolder should be set to InputFolder for automatic annotation importation

**Note**: Except for last case, ExportFolder is typically set to ReportFolder

**IA Server (JULI)**

>> JULI(MonitoredFolder, PathToLogFile, 'user@gmail.com','password'); Launch server

Should be provided in job:

Dstmail = '[youremail@youremailprovider.com](mailto:youremail@youremailprovider.com)';

AttachmentFolder: typically set to ReportFolder, can be undefined for no attachment

**Journal processing options (common to 2D/3D journals)**

**Rescale**  >=1 Downscaling factor prior to processing (default = 1)

**ExportDist** 0 Do not export mask distance map (default)

1 Export distance map (outside objects)

2 Export distance map (inside objects)

(Distance map: any pixel >1 is object)

Note: For 3D journals, distance map is computed on image **O** unless image **M** is defined.

**Dilate** >=1 Integer**,** 2Ddilate objects in mask (pix)

**2D journals (.jl) specific processing options**

**MinLocalFocus** Do not process image if focus score smaller than this value

**LocalFocusBlkSize** Block size (pix) used to compute local focus score

**Min95Percentile** Minimum maximum intensity excluding 5% brightest pixels

**MaxSatPixFract** Maximum fraction of saturated pixels

Following options are display only:

**Lbl** 0 Display binary mask overlay

1 Display label mask overlay (colours)

**Fill** -1 Original mask (no contouring, no dilation)

0 Mask contour, apply dilation (default)

1 Original mask + dilation

**3D journals (.jls) specific processing options**

**Step** Process only each **Step** images in stack (default = 1)

**Offset** Start at image **Offset** in stack (default = 0)

**SaveOutput** If set to 1, output variable **O** is saved to output folder (default = 0)

**Brick** Brick XY size, defining this variable enables brick mode

**GuardBand** Overlap in pixels between XY bricks to avoid border effects (default = 64 pix)

**FoldersIn** Set to 1 if input images are folders of 2D images (default = 0)

Following options are display only

**NCols** Sets number of random colours in palette for label masks (default = 16)

**PointSize** For 3D rendering, sets size of displayed points (default = 1)

**RunProj** If set >1, running local maximum intensity Z projection is performed (**RunProj** slices are locally projected). Ignored for 3D rendering (default = 1)

**ZRatio** For 3D rendering, Z slices to pixel size ratio (default = 1)

**Shw**  Control input and output image stacks display (see below).

**0** Display input and output images in two separate slice browsers

**1** Overlay output **binary mask** over input image

**2** Overlay output binary or label mask contours over input image

**3** Overlay output label mask over input image (if binary mask detected, connected component analysis is performed to label objects)

**4** Output volume rendering

**5** Input volume rendering + output mask overlay as surface points mesh

**Time-lapse journals (.jlm) specific processing options**

**Shw**  -1 No display

1. Display label mask overlaid on input image

2 Display only output image

**Slice browser controls**

**Mask tick box** Show / hide mask overlay

**Intensity** Mouse position and image intensity + mask values (lower left corner)

**Contrast** Left click + move mouse up/down - left/right to adjust intensity display. Lower and higher clipping values are displayed as **L** (lower) and **W** (higher) and can also be user defined by clicking them.

**Histogram** Tick histogram to view image histogram

**ROIs** Intensity measurements can be performed by drawing ROIs with tools

**Colours** Use drop down menu on the left of floppy disk to change image LUT

**Zoom in/out** Press shift + left click + move mouse

**Reset view** Use landscape button to reset view

**Slice selection** Use slider on left side or mouse wheel to scroll though slices

**Grid** Use tick box to display / hide grid

**‘x’** Resume processing

**‘r’** Launch 3D renderer (draw bounding box, adjust depth before with **z**)

**‘z’** Set number of slices used for local z projection

**‘m’** Toggle mask overlay

**3D renderer controls**

**m** Show/hide point mesh overlay

**c** Display min/max intensity value clipping dialog

**space** Reset view

**Close window** Resume processing

**Seeds mask measurements (‘Spts’)**

**Centroid** X,Y(,Z) object position

**MeanInt** Mean intensity

**Skeletons mask measurements (‘Skls’)**

**sklvol** Number of pixels (voxels) of the skeleton

**skllgth** Total skeleton (min 1 branch) length (XY pixel unit), Z ratio corrected

**sklbrpts** Number of skeleton branch points

**sklenpts** Number of skeleton end points

**objvol** Volume of the segmentation mask prior to skeletonization (pix or vox), if found

**imgvol** Image volume (pix or vox)

**meanint** Mean intensityof skeleton voxels in intensity channel(s)

**histint** Histogram(bins centred on [1:16]) of skeleton voxels in intensity channel(s)

**Objects mask measurements (‘Objs’)**

**Area** Object area/volume

**Centroid** X,Y(,Z) position

**Bounding Box** X,Y(,Z) position of top upper left corner + width, height(,depth)

**MeanInt** Average intensity inside object in intensity channel(s)

**NonNullPix** Number of non-null pixel inside object in intensity channel(s)

**Moving Objects mask (‘Trks’)**

**Area** Object area/volume at each time point

**Centroid** X,Y,(Z) object position at each time point

**MeanInt** Average intensity inside object in intensity channel(s) at each time point

**Dual mask measurements (IRMA third argument: ‘Spst’)**

**Ovl**  2nd numeric value of 5th IRMA argument: {ZRatio, Ovl, ‘’}

**Dice** Dice coefficient between both masks

**Dice\_ovl** Dice coefficient between both masks after dilation by **Ovl** pixels

**Frnd** Expected fraction of co-localized pixels (uniform distribution in free regions)

**Fobs** Observed fraction of co-localized pixels

**Pobs** Probability of observation for uniform distribution in free regions

**alpha** Co-localization probability factor: P(r+|g+) / P(r+|g-)

**beta** Exclusion probability factor: P(r-|g+) / P(r-|g-)

**FN** False negative: count of objects present in channel A and not in channel B

**FP** False positive: count of objects present in channel B and not in channel A

**TP** True positive: count of objects present in both channels

**clustA** Objects A area divided by number of objects A after mask dilation

**custB** Objects B area divided by number of objects B after mask dilation

Notes:

Low Pobs (e.g < 1%) hint toward co-localization or exclusion since in both cases the observation will deviate from the free distribution scenario. To conclude on co-localization or exclusion, one should compare **Fobs** to **Pobs**.

**Masks grayscale levels**

**Object mask** (8-bit image)

|  |  |
| --- | --- |
| **0** | background |
| **255** | foreground |

**Object label mask** (16-bit image)

|  |  |
| --- | --- |
| **0** | background |
| **1-65535** | object label |

**Seed mask** (8-bit image)

|  |  |
| --- | --- |
| **0** | background |
| **100** | optional mask (spot segmentation) |
| **200** | plain seeds (1 pixel markers) |
| **220-250** | classified seeds |

**Skeleton mask** (8-bit image)

|  |  |
| --- | --- |
| **0** | background |
| **100** | optional mask (filament segmentation) |
| **200** | skeleton (1 pixel central axis) |
| **220** | skeleton end point |
| **250** | skeleton branch point |